

The diagram illustrates the process of identifying truly unique primers from a sequence of repeats. It starts with a sequence of 12 nucleotides: A, B, C, R, A, X, D, Y, D, E, F, R, A, R. The first 12 nucleotides are grouped into a box labeled "Region of Interest". The sequence is then processed through several steps:

- Mask Repeats:** The sequence is processed to mask repeats, resulting in a sequence where the first 12 nucleotides are masked (represented by 'X' in the original image) and the remaining 12 nucleotides are 'Y, D, E, F, R, A, R'.
- Discard Non-unique:** The sequence is processed to discard non-unique primers, resulting in a sequence where the first 12 nucleotides are masked (represented by 'X' in the original image) and the remaining 12 nucleotides are 'Y, D, E, F, R, A, R'.
- Design Truly Unique Primers:** The sequence is processed to design truly unique primers, resulting in a sequence where the first 12 nucleotides are masked (represented by 'X' in the original image) and the remaining 12 nucleotides are 'Y, D, E, F, R, A, R'.

The final sequence is labeled "R=Repeats".

FIG. 1

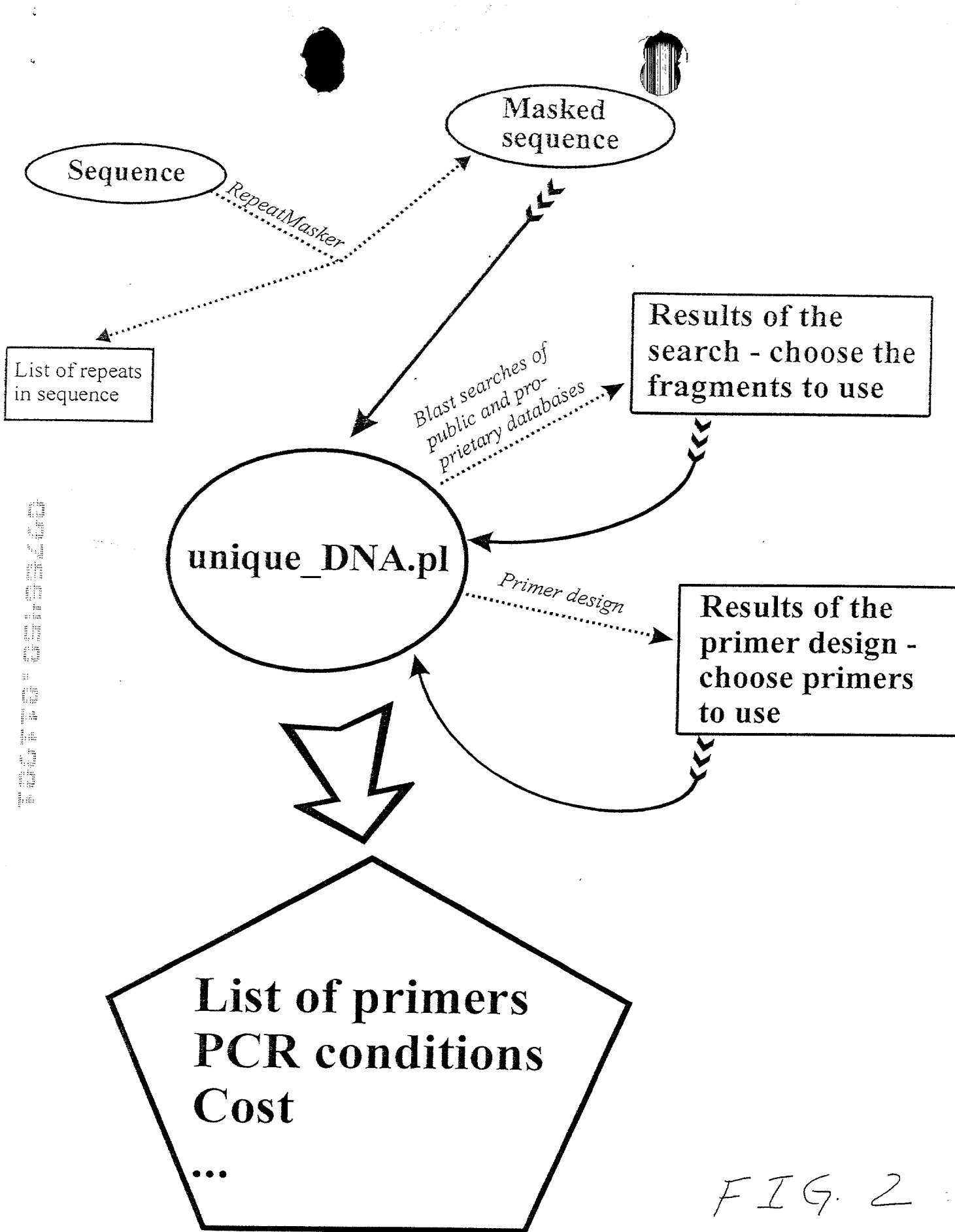


FIG. 2